

10/590705

SEQUENCE LISTING

<110> KYOWA HAKKO KOGYO CO., LTD

<120> Method for producing amino acid

<130> 1657

<160> 16

<170> PatentIn Ver. 3.1

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<211> 30

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48

gtc atc ggt tct ggt ttt ggt ggc ctt ttt gct gcc aag aac ctg gcc

Val Ile Gly Ser Gly Phe Gly Leu Phe Ala Ala Lys Asn Leu Ala

20

25

30

96

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ttc	cag	cca	ctg	ctg	tac	caa	gtg	gca	acc	ggt	atc	ctc	tcc	tcc	ggt	192
Phe	Gln	Pro	Leu	Leu	Tyr	Gln	Val	Ala	Thr	Gly	Ile	Leu	Ser	Ser	Gly	
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gaa	atc	gca	cct	tcc	act	cga	cag	atc	ctg	ggc	tcc	cag	gaa	aac	gtc	240
Glu	Ile	Ala	Pro	Ser	Thr	Arg	Gln	Ile	Leu	Gly	Ser	Gln	Glu	Asn	Val	
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aac	gtc	atc	aag	ggc	gaa	gtc	acc	gac	atc	aac	gtc	gag	tcc	cag	act	288
Asn	Val	Ile	Lys	Gly	Glu	Val	Thr	Asp	Ile	Asn	Val	Glu	Ser	Gln	Thr	
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gtg	acc	gcc	tcc	ctg	ggc	gag	ttc	acc	cgc	gtt	ttt	gag	tac	gat	tcc	336
Val	Thr	Ala	Ser	Leu	Gly	Glu	Phe	Thr	Arg	Val	Phe	Glu	Tyr	Asp	Ser	
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Leu	Val	Val	Gly	Ala	Gly	Ala	Gly	Gln	Ser	Tyr	Phe	Gly	Asn	Asp	His	
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Phe	Ala	Glu	Phe	Ala	Pro	Gly	Met	Lys	Ser	Ile	Asp	Asp	Ala	Leu	Glu	
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Ile	Arg	Ala	Arg	Ile	Ile	Gly	Ala	Phe	Glu	Arg	Ala	Glu	Ile	Cys	Glu	
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gat	cca	gct	gag	cgc	gaa	cgc	ctg	ctc	acc	ttc	gtc	gtt	gtt	ggc	gct	528
Asp	Pro	Ala	Glu	Arg	Glu	Arg	Leu	Leu	Thr	Phe	Val	Val	Val	Gly	Ala	
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Gly	Pro	Thr	Gly	Val	Glu	Leu	Ala	Gly	Gln	Leu	Ala	Glu	Met	Ala	His	
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cgc	acc	ctt	gct	ggt	gag	tac	aag	aac	ttc	aac	acc	aac	tcc	gca	aag	624
Arg	Thr	Leu	Ala	Gly	Glu	Tyr	Lys	Asn	Phe	Asn	Thr	Asn	Ser	Ala	Lys	
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atc	atc	ctg	ctt	gat	ggt	gct	cca	cag	gtt	ctt	cct	cca	ttc	ggt	aag	672
Ile	Ile	Leu	Leu	Asp	Gly	Ala	Pro	Gln	Val	Leu	Pro	Pro	Phe	Gly	Lys	
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Arg Leu Gly Arg Asn Ala Gln Arg Thr Leu Glu Lys Met Gly Val Asn
225 230 235 240

gtt cgc ctg aac gct atg gtc acc aac gtt gac gct acc tcg gtc acc 768
Val Arg Leu Asn Ala Met Val Thr Asn Val Asp Ala Thr Ser Val Thr
245 250 255

tac aag acc aag gac ggc gaa gag cac acc atc gaa tct ttc tgc aag 816
Tyr Lys Thr Lys Asp Gly Glu His Thr Ile Glu Ser Phe Cys Lys
260 265 270

att tgg tcc gct ggt gtt gcg gca tcc cca ctg ggc aag ctc gtc gca 864
Ile Trp Ser Ala Gly Val Ala Ser Pro Leu Gly Lys Leu Val Ala
275 280 285

gag cag acc ggt gtt gag acc gac cgc gca ggc cgc gtc atg gtt aac 912
Glu Gln Thr Gly Val Glu Thr Asp Arg Ala Gly Arg Val Met Val Asn
290 295 300

gat gac ctg tct gtt ggc gat cag aag aac gtc ttc gtt gtt ggc gac 960
Asp Asp Leu Ser Val Gly Asp Gln Lys Asn Val Phe Val Val Gly Asp
305 310 315 320

atg atg aac tac aac aac ctc cct ggt gtt gct cag gta gca atc cag
1008
Met Met Asn Tyr Asn Asn Leu Pro Gly Val Ala Gln Val Ala Ile Gln
325 330 335

agt ggt gag tac gtt gct gag cag atc gaa gct gag gtt gaa ggc cgc
1056
Ser Gly Glu Tyr Val Ala Glu Gln Ile Glu Ala Glu Val Glu Gly Arg
340 345 350

tcc aac acc gag cgc gaa gct ttc gat tac ttc gac aag ggc tcc atg
1104
Ser Asn Thr Glu Arg Glu Ala Phe Asp Tyr Phe Asp Lys Gly Ser Met
355 360 365

gct acc att tcc cgc ttc tcc gca gtg gtg aag atg ggc aag gtt gag
1152
Ala Thr Ile Ser Arg Phe Ser Ala Val Val Lys Met Gly Lys Val Glu
370 375 380

gtc acc ggc ttc atc ggt tgg gtt ctg tgg ttg gct gtt cac atc atg
1200
Val Thr Gly Phe Ile Gly Trp Val Leu Trp Leu Ala Val His Ile Met
385 390 395 400

ttc ctg gtt ggc ttc cgc aac cgt ttc gtc tcc gca atc agc tgg ggc
1248

Phe Leu Val Gly Phe Arg Asn Arg Phe Val Ser Ala Ile Ser Trp Gly
405 410 415

ctg aac gca ctg tcc cgc aag cgt tgg aac ctg gca acc acc cgc cag
1296

Leu Asn Ala Leu Ser Arg Lys Arg Trp Asn Leu Ala Thr Thr Arg Gln
420 425 430

cag ctc cac tca cgc acc acg ctg tcc aag ttc gct cac gag ctt gag
1344

Gln Leu His Ser Arg Thr Thr Leu Ser Lys Phe Ala His Glu Leu Glu
435 440 445

gaa gca tct tct gat ctt cca atc gag ctg cgc gac aac cag cgt ttc
1392

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1404

Ser Gly Lys

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<212> PRT

<213> Corynebacterium glutamicum ATCC13032

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35 40 45

Phe Gln Pro Leu Leu Tyr Gln Val Ala Thr Gly Ile Leu Ser Ser Gly
50 55 60

Glu Ile Ala Pro Ser Thr Arg Gln Ile Leu Gly Ser Gln Glu Asn Val
65 70 75 80

Asn Val Ile Lys Gly Glu Val Thr Asp Ile Asn Val Glu Ser Gln Thr
85 90 95

Val Thr Ala Ser Leu Gly Glu Phe Thr Arg Val Phe Glu Tyr Asp Ser
100 105 110

Leu Val Val Gly Ala Gly Ala Gly Gln Ser Tyr Phe Gly Asn Asp His
115 120 125

Phe Ala Glu Phe Ala Pro Gly Met Lys Ser Ile Asp Asp Ala Leu Glu
130 135 140

Ile Arg Ala Arg Ile Ile Gly Ala Phe Glu Arg Ala Glu Ile Cys Glu
145 150 155 160

Asp Pro Ala Glu Arg Glu Arg Leu Leu Thr Phe Val Val Val Gly Ala
165 170 175

Gly Pro Thr Gly Val Glu Leu Ala Gly Gln Leu Ala Glu Met Ala His
180 185 190

Arg Thr Leu Ala Gly Glu Tyr Lys Asn Phe Asn Thr Asn Ser Ala Lys
195 200 205

Ile Ile Leu Leu Asp Gly Ala Pro Gln Val Leu Pro Pro Phe Gly Lys
210 215 220

Arg Leu Gly Arg Asn Ala Gln Arg Thr Leu Glu Lys Met Gly Val Asn
225 230 235 240

Val Arg Leu Asn Ala Met Val Thr Asn Val Asp Ala Thr Ser Val Thr
245 250 255

Tyr Lys Thr Lys Asp Gly Glu Glu His Thr Ile Glu Ser Phe Cys Lys
260 265 270

Ile Trp Ser Ala Gly Val Ala Ala Ser Pro Leu Gly Lys Leu Val Ala
275 280 285

Glu Gln Thr Gly Val Glu Thr Asp Arg Ala Gly Arg Val Met Val Asn
290 295 300

Asp Asp Leu Ser Val Gly Asp Gln Lys Asn Val Phe Val Val Gly Asp
305 310 315 320

Met Met Asn Tyr Asn Asn Leu Pro Gly Val Ala Gln Val Ala Ile Gln
325 330 335

Ser Gly Glu Tyr Val Ala Glu Gln Ile Glu Ala Glu Val Glu Gly Arg
340 345 350

Ser Asn Thr Glu Arg Glu Ala Phe Asp Tyr Phe Asp Lys Gly Ser Met
355 360 365

Ala Thr Ile Ser Arg Phe Ser Ala Val Val Lys Met Gly Lys Val Glu

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Leu Asn Ala Leu Ser Arg Lys Arg Trp Asn Leu Ala Thr Thr Arg Gln			
420	425	430	
Gln Leu His Ser Arg Thr Thr Leu Ser Lys Phe Ala His Glu Leu Glu			
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Arg	Thr	Leu	Ser	Gly	Glu	Tyr	Thr	Gln	Phe	Thr	Pro	Ser	Asn	Ala	Lys	
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atc	atc	ctg	ctt	gac	ggc	gct	cct	cag	gtg	ctt	cca	ccg	ttc	ggc	aag	672
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gtc	aag	ctg	aac	gct	atc	gtt	acc	ggc	gta	gac	gaa	aac	tca	gtg	aca	768
Val	Lys	Leu	Asn	Ala	Ile	Val	Thr	Gly	Val	Asp	Glu	Asn	Ser	Val	Thr	
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Tyr	Lys	Ser	Thr	Val	Asp	Asp	Ser	Leu	His	Thr	Ile	Asp	Ser	Phe	Cys	
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275 280 285

gca gag cag ctt ggt gtc gag gtt gat cgt gca gga cgc gtc cca gtc 912
Ala Glu Gln Leu Gly Val Glu Val Asp Arg Ala Gly Arg Val Pro Val
290 295 300

aac gaa gat ctt tct gtt ggc gac gat aag aac gtc ttt gtt att ggc 960
Asn Glu Asp Leu Ser Val Gly Asp Asp Lys Asn Val Phe Val Ile Gly
305 310 315 320

gat atg atg tcg ctc aac agg ctt ccg gga gtc gca cag gta gca atc
1008
Asp Met Met Ser Leu Asn Arg Leu Pro Gly Val Ala Gln Val Ala Ile
325 330 335

caa ggc ggt gaa tac gtt gct gag cag att gct gct ggg gtc gag gga
1056
Gln Gly Gly Glu Tyr Val Ala Glu Gln Ile Ala Ala Gly Val Glu Gly
340 345 350

cgt tcc tcg tct gaa cgc cca gcc ttt gaa tac tac gac aag ggt tcg
1104
Arg Ser Ser Ser Glu Arg Pro Ala Phe Glu Tyr Tyr Asp Lys Gly Ser
355 360 365

atg gct acg gtg tcg cgc ttt aac gcc gtt gtg aag ctt gga aaa gtt
1152
Met Ala Thr Val Ser Arg Phe Asn Ala Val Val Lys Leu Gly Lys Val
370 375 380

gaa gtt acg gga ttt att ggc tgg gtc atg tgg ctt ctc gtc cac ttg
1200
Glu Val Thr Gly Phe Ile Gly Trp Val Met Trp Leu Leu Val His Leu
385 390 395 400

atg ttc ttg gtc ggc ttc cgc aac cga gca act gcg gct ttc tct tgg
1248
Met Phe Leu Val Gly Phe Arg Asn Arg Ala Thr Ala Ala Phe Ser Trp
405 410 415

ggc atc aat gcg ctt tca cgt aag cgt tgg aac ctc gcc acc act cgt
1296
Gly Ile Asn Ala Leu Ser Arg Lys Arg Trp Asn Leu Ala Thr Thr Arg
420 425 430

cag cag ctt cac ggc cgt act ggt ttg caa aaa ctt act gcg ctc gtc
1344
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435

440

445

1362

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Asp Ala Asp Val Asp Ile Thr Leu Ile Asp Arg Thr Asn His His Leu
 35 40 45

Phe Gln Pro Leu Leu Tyr Gln Val Ala Thr Gly Ile Leu Ser Ser Gly
 50 55 60

Glu Ile Ala Pro Gln Thr Arg Gln Val Leu Ala Gln Gln Asn Asn Val
 65 70 75 80

His Val Leu Lys Ala Glu Val Thr Asp Ile Asp Thr Glu Ser Lys Thr
 85 90 95

Val Val Ala Asp Leu Asp Asp Tyr Ser Lys Thr Ile Glu Tyr Asp Ser
 100 105 110

Leu Ile Val Ala Ala Gly Ala Gly Gln Ser Tyr Phe Gly Asn Asp His
 115 120 125

Phe Ala Glu Phe Ala Pro Gly Met Lys Thr Ile Asp Asp Ala Leu Glu
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Leu Arg Ala Arg Ile Ile Gly Ala Phe Glu Arg Ala Glu Met Cys Glu
 145 150 155 160

Asp Pro Lys Glu Arg Glu Arg Leu Leu Thr Phe Val Ile Val Gly Ala
 165 170 175

Gly Pro Thr Gly Val Glu Leu Ala Gly Gln Leu Ala Glu Met Ala His
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Arg Thr Leu Ser Gly Glu Tyr Thr Gln Phe Thr Pro Ser Asn Ala Lys
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Ile Ile Leu Leu Asp Gly Ala Pro Gln Val Leu Pro Pro Phe Gly Lys
210 215 220

Arg Leu Gly Arg Thr Ala Gln Arg Glu Leu Glu Lys Ile Gly Val Thr
225 230 235 240

Val Lys Leu Asn Ala Ile Val Thr Gly Val Asp Glu Asn Ser Val Thr
245 250 255

Tyr Lys Ser Thr Val Asp Asp Ser Leu His Thr Ile Asp Ser Phe Cys
260 265 270

Lys Ile Trp Ser Ala Gly Val Ala Ala Ser Pro Leu Gly Lys Leu Val
275 280 285

Ala Glu Gln Leu Gly Val Glu Val Asp Arg Ala Gly Arg Val Pro Val
290 295 300

Asn Glu Asp Leu Ser Val Gly Asp Asp Lys Asn Val Phe Val Ile Gly
305 310 315 320

Asp Met Met Ser Leu Asn Arg Leu Pro Gly Val Ala Gln Val Ala Ile
325 330 335

Gln Gly Gly Glu Tyr Val Ala Glu Gln Ile Ala Ala Gly Val Glu Gly
340 345 350

Arg Ser Ser Ser Glu Arg Pro Ala Phe Glu Tyr Tyr Asp Lys Gly Ser
355 360 365

Met Ala Thr Val Ser Arg Phe Asn Ala Val Val Lys Leu Gly Lys Val
370 375 380

Glu Val Thr Gly Phe Ile Gly Trp Val Met Trp Leu Leu Val His Leu
385 390 395 400

Met Phe Leu Val Gly Phe Arg Asn Arg Ala Thr Ala Ala Phe Ser Trp
405 410 415

Gly Ile Asn Ala Leu Ser Arg Lys Arg Trp Asn Leu Ala Thr Thr Arg
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<213> Escherichia coli

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Gly Leu Glu Met Ala Thr Gln Leu Gly His Lys Leu Gly Arg Lys Lys
20 25 30

aaa gcc aaa att acg ctg gtc gat cgt aac cac agc cac ctg tgg aaa 144
Lys Ala Lys Ile Thr Leu Val Asp Arg Asn His Ser His Leu Trp Lys
35 40 45

ccg ctg ctg cac gaa gtc gcg act ggc tcg ctt gat gaa ggc gtc gat 192
Pro Leu Leu His Glu Val Ala Thr Gly Ser Leu Asp Glu Gly Val Asp
50 55 60

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Leu Gly Ser Val Ile Asp Ile Asp Arg Glu Ala Lys Thr Ile Thr Ile
85 90 95

gca gaa ctg cgc gac gag aaa ggt gaa ctg ctg gtt ccg gaa cgt aaa 336
Ala Glu Leu Arg Asp Glu Lys Gly Glu Leu Leu Val Pro Glu Arg Lys
100 105 110

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Ile Ala Tyr Asp Thr Leu Val Met Ala Leu Gly Ser Thr Ser Asn Asp
115 120 125

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Phe Asn Thr Pro Gly Val Lys Glu Asn Cys Ile Phe Leu Asp Asn Pro
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145 150 155 160

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Gly	Gly	Gly	Ala	Thr	Gly	Val	Glu	Leu	Ser	Ala	Glu	Leu	His	Asn	Ala		
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225									230					235		240	
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Val	Arg	Val	Leu	Thr	Gln	Thr	Met	Val	Thr	Ser	Ala	Asp	Glu	Gly	Gly		
245									250						255		
ctg	cac	act	aaa	gat	ggc	gaa	tat	att	gag	gct	gat	ctg	atg	gta	tgg	816	
Leu	His	Thr	Lys	Asp	Gly	Glu	Tyr	Ile	Glu	Ala	Asp	Leu	Met	Val	Trp		
260									265						270		
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275									280						285		
gaa	act	aac	cgt	atc	aac	cag	ctg	gtg	gtg	gaa	ccg	acg	ctg	caa	acc	912	
Glu	Thr	Asn	Arg	Ile	Asn	Gln	Leu	Val	Val	Glu	Pro	Thr	Leu	Gln	Thr		
290									295					300			
acc	cgc	gat	cca	gac	att	tac	gct	att	ggc	gac	tgc	gcf	tca	tgc	ccg	960	
Thr	Arg	Asp	Pro	Asp	Ile	Tyr	Ala	Ile	Gly	Asp	Cys	Ala	Ser	Cys	Pro		
305									310						315		320
cgt	ccg	gaa	ggg	ggc	ttt	gtt	ccg	ccg	cgt	gct	cag	gct	gca	cac	cag		
1008																	
Arg	Pro	Glu	Gly	Gly	Phe	Val	Pro	Pro	Arg	Ala	Gln	Ala	Ala	His	Gln		
325															335		
atg	gcf	act	tgc	gca	atg	aac	aac	att	ctg	gcf	cag	atg	aac	ggt	aag		
1056																	
Met	Ala	Thr	Cys	Ala	Met	Asn	Asn	Ile	Leu	Ala	Gln	Met	Asn	Gly	Lys		
340									345						350		

ccg ctg aaa aat tat cag tat aaa gat cat ggt tcg ctg gta tcg ctg
1104
Pro Leu Lys Asn Tyr Gln Tyr Lys Asp His Gly Ser Leu Val Ser Leu
355 360 365

tcg aac ttc tcc acc gtc ggt agc ctg atg ggt aac ctg acg cgc ggc
1152
Ser Asn Phe Ser Thr Val Gly Ser Leu Met Gly Asn Leu Thr Arg Gly
370 375 380

tca atg atg att gaa gga cga att gcg cgc ttt gta tat atc tcg cta
1200
Ser Met Met Ile Glu Gly Arg Ile Ala Arg Phe Val Tyr Ile Ser Leu
385 390 395 400

tac cga atg cat cag att gcg ctg cat ggt tac ttt aaa acc gga tta
1248
Tyr Arg Met His Gln Ile Ala Leu His Gly Tyr Phe Lys Thr Gly Leu
405 410 415

atg atg ctg gtg ggg agt att aac cgc gtt atc cgt ccg cgt ttg aag
1296
Met Met Leu Val Gly Ser Ile Asn Arg Val Ile Arg Pro Arg Leu Lys
420 425 430

ttg cat 1302
Leu His

<210> 8
<211> 434
<212> PRT
<213> Escherichia coli

<400> 8
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1 5 10 15

Gly Leu Glu Met Ala Thr Gln Leu Gly His Lys Leu Gly Arg Lys Lys
20 25 30

Lys Ala Lys Ile Thr Leu Val Asp Arg Asn His Ser His Leu Trp Lys
35 40 45

Pro Leu Leu His Glu Val Ala Thr Gly Ser Leu Asp Glu Gly Val Asp
50 55 60

Ala Leu Ser Tyr Leu Ala His Ala Arg Asn His Gly Phe Gln Phe Gln
65 70 75 80

Leu Gly Ser Val Ile Asp Ile Asp Arg Glu Ala Lys Thr Ile Thr Ile

85 90 95

Ala Glu Leu Arg Asp Glu Lys Gly Glu Leu Leu Val Pro Glu Arg Lys
100 105 110

Ile Ala Tyr Asp Thr Leu Val Met Ala Leu Gly Ser Thr Ser Asn Asp
115 120 125

Phe Asn Thr Pro Gly Val Lys Glu Asn Cys Ile Phe Leu Asp Asn Pro
130 135 140

His Gln Ala Arg Arg Phe His Gln Glu Met Leu Asn Leu Phe Leu Lys
145 150 155 160

Tyr Ser Ala Asn Leu Gly Ala Asn Gly Lys Val Asn Ile Ala Ile Val
165 170 175

Gly Gly Gly Ala Thr Gly Val Glu Leu Ser Ala Glu Leu His Asn Ala
180 185 190

Val Lys Gln Leu His Ser Tyr Gly Tyr Lys Gly Leu Thr Asn Glu Ala
195 200 205

Leu Asn Val Thr Leu Val Glu Ala Gly Glu Arg Ile Leu Pro Ala Leu
210 215 220

Pro Pro Arg Ile Ser Ala Ala Ala His Asn Glu Leu Thr Lys Leu Gly
225 230 235 240

Val Arg Val Leu Thr Gln Thr Met Val Thr Ser Ala Asp Glu Gly Gly
245 250 255

Leu His Thr Lys Asp Gly Glu Tyr Ile Glu Ala Asp Leu Met Val Trp
260 265 270

Ala Ala Gly Ile Lys Ala Pro Asp Phe Leu Lys Asp Ile Gly Gly Leu
275 280 285

Glu Thr Asn Arg Ile Asn Gln Leu Val Val Glu Pro Thr Leu Gln Thr
290 295 300

Thr Arg Asp Pro Asp Ile Tyr Ala Ile Gly Asp Cys Ala Ser Cys Pro
305 310 315 320

Arg Pro Glu Gly Gly Phe Val Pro Pro Arg Ala Gln Ala Ala His Gln
325 330 335

Met Ala Thr Cys Ala Met Asn Asn Ile Leu Ala Gln Met Asn Gly Lys
340 345 350

Pro Leu Lys Asn Tyr Gln Tyr Lys Asp His Gly Ser Leu Val Ser Leu
355 360 365

Ser Asn Phe Ser Thr Val Gly Ser Leu Met Gly Asn Leu Thr Arg Gly
370 375 380

Ser Met Met Ile Glu Gly Arg Ile Ala Arg Phe Val Tyr Ile Ser Leu
385 390 395 400

Tyr Arg Met His Gln Ile Ala Leu His Gly Tyr Phe Lys Thr Gly Leu
405 410 415

Met Met Leu Val Gly Ser Ile Asn Arg Val Ile Arg Pro Arg Leu Lys
420 425 430

Leu His

<210> 9

<211> 1296

<212> DNA

<213> Pseudomonas fluorescens

<220>

<221> CDS

<222>

<400> 9

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Met Thr His Arg Ile Val Ile Val Gly Gly Ala Gly Gly Leu Glu
1 5 10 15

ttg gct acc cgt ctg ggt aag act ctg ggc aag cgt ggc acg gcc agt 96
Leu Ala Thr Arg Leu Gly Lys Thr Leu Gly Lys Arg Gly Thr Ala Ser
20 25 30

gtg atg ctg gtc gac gcg aac ctg acc cac atc tgg aaa ccg cta ctg 144
Val Met Leu Val Asp Ala Asn Leu Thr His Ile Trp Lys Pro Leu Leu
35 40 45

cac gaa gtg gcc gcc ggc tcc ttg aac tcc tcc gaa gac gaa ctc aac 192
His Glu Val Ala Ala Gly Ser Leu Asn Ser Ser Glu Asp Glu Leu Asn
50 55 60

tat gtc gcc cag gca aaa tgg aac cac ttc gag ttc cag ctc ggg cgc 240
Tyr Val Ala Gln Ala Lys Trp Asn His Phe Glu Phe Gln Leu Gly Arg
65 70 75 80

atg agc ggc ctg gat cgc gag cgc aag aga atc caa ctg gcc gcc acc 288
Met Ser Gly Leu Asp Arg Glu Arg Lys Arg Ile Gln Leu Ala Ala Thr

85	90	95	
tat gac gag acc ggc gtc gag ctg ttg ccg gcc cg ^g gaa ctg ggc tac Tyr Asp Glu Thr Gly Val Glu Leu Leu Pro Ala Arg Glu Leu Gly Tyr 100	105	110	336
gac acc ctg gtg att gcc gtc ggc agc acc acc aat gac ttc ggc acc Asp Thr Leu Val Ile Ala Val Gly Ser Thr Thr Asn Asp Phe Gly Thr 115	120	125	384
gaa ggc gcg gcg cag cac tgc ctg ttc ctc gac acc cgc aaa cag gcc Glu Gly Ala Ala Gln His Cys Leu Phe Leu Asp Thr Arg Lys Gln Ala 130	135	140	432
gag cgc ttc cat cag c ^a aa ttg ctg cac cac tat ctg cgc gcc cac gcc Glu Arg Phe His Gln Gln Leu Leu His His Tyr Leu Arg Ala His Ala 145	150	155	480
ggg cag acc gat atc gtc gag cgc atc agc gtc gcc att gtc ggc gcc Gly Gln Thr Asp Ile Val Glu Arg Ile Ser Val Ala Ile Val Gly Ala 165	170	175	528
ggt gcg acc ggg gtc gaa ctg gcc gag ctg cat aat gcc gcc cac Gly Ala Thr Gly Val Glu Leu Ala Ala Glu Leu His Asn Ala Ala His 180	185	190	576
gaa ctg cac gcc tac ggc ctg gac cgg atc aaa ccg gag aac atg cac Glu Leu His Ala Tyr Gly Leu Asp Arg Ile Lys Pro Glu Asn Met His 195	200	205	624
atc acc ctg atc gag gcc ggg cca cgc gtc ttg ccg gcc ctg ccg gag Ile Thr Leu Ile Glu Ala Gly Pro Arg Val Leu Pro Ala Leu Pro Glu 210	215	220	672
cgt atc ggc ggg ccg gtg cac aag acc ctg gaa aaa ctc ggg gtc aac Arg Ile Gly Gly Pro Val His Lys Thr Leu Glu Lys Leu Gly Val Asn 225	230	235	720
gtc atg acc aac gcc gcc gtc agc cag gtg acc gcc gac agc ctg att Val Met Thr Asn Ala Ala Val Ser Gln Val Thr Ala Asp Ser Leu Ile 245	250	255	768
acc gcg gac ggc aaa gtg atc gac gcg agc ctg aaa gtc tgg gcc gcc Thr Ala Asp Gly Lys Val Ile Asp Ala Ser Leu Lys Val Trp Ala Ala 260	265	270	816
ggg att cgc gcc ccg gac ttc ctc aag gac atc gac ggg ctg gag acc Gly Ile Arg Ala Pro Asp Phe Leu Lys Asp Ile Asp Gly Leu Glu Thr 275	280	285	864

aac cggtatc aac cag ttg cac gtg ctg ccc act ttg cag acc acc cgc 912
Asn Arg Ile Asn Gln Leu His Val Leu Pro Thr Leu Gln Thr Thr Arg
290 295 300

gac gag aac atc ttc gcc ttc ggc gac tgc gcc gcc tgc ccg caa ccc 960
Asp Glu Asn Ile Phe Ala Phe Gly Asp Cys Ala Ala Cys Pro Gln Pro
305 310 315 320

ggc agc gag cgc aac gtc cca cct cgc gcc cag gcc gca cac cag caa
1008
Gly Ser Glu Arg Asn Val Pro Pro Arg Ala Gln Ala Ala His Gln Gln
325 330 335

gcc tca ctg ctg gcc aaa tcc ttg aag ctg cgg atc gag ggc aag gcc
1056
Ala Ser Leu Leu Ala Lys Ser Leu Lys Leu Arg Ile Glu Gly Lys Ala
340 345 350

ctg ccg gaa tac aaa tac acc gac tac ggc tcg ctg atc tcg ctg tcg
1104
Leu Pro Glu Tyr Lys Tyr Thr Asp Tyr Gly Ser Leu Ile Ser Leu Ser
355 360 365

cgg ttc tcg gca gtg ggc aac ctg atg ggt aac ctg acc ggc agc gtg
1152
Arg Phe Ser Ala Val Gly Asn Leu Met Gly Asn Leu Thr Gly Ser Val
370 375 380

atg ctc gaa ggc tgg ctg gcg cgg atg ttc tat gtg tcg ctg tac cgc
1200
Met Leu Glu Gly Trp Leu Ala Arg Met Phe Tyr Val Ser Leu Tyr Arg
385 390 395 400

atg cac cag atg gcg ctg tac ggc atg ttc cgc acg gcc atg ttg atg
1248
Met His Gln Met Ala Leu Tyr Gly Met Phe Arg Thr Ala Met Leu Met
405 410 415

ctg ggt agc aag atc ggg cgt ggg acc gag cct cgg ctg aag ctg cac
1296
Leu Gly Ser Lys Ile Gly Arg Gly Thr Glu Pro Arg Leu Lys Leu His
420 425 430

<210> 10
<211> 432
<212> PRT
<213> Pseudomonas fluorescens

<400> 10
Met Thr His Arg Ile Val Ile Val Gly Gly Gly Ala Gly Gly Leu Glu

1 5 10 15
Leu Ala Thr Arg Leu Gly Lys Thr Leu Gly Lys Arg Gly Thr Ala Ser
20 25 30
Val Met Leu Val Asp Ala Asn Leu Thr His Ile Trp Lys Pro Leu Leu
35 40 45
His Glu Val Ala Ala Gly Ser Leu Asn Ser Ser Glu Asp Glu Leu Asn
50 55 60
Tyr Val Ala Gln Ala Lys Trp Asn His Phe Glu Phe Gln Leu Gly Arg
65 70 75 80
Met Ser Gly Leu Asp Arg Glu Arg Lys Arg Ile Gln Leu Ala Ala Thr
85 90 95
Tyr Asp Glu Thr Gly Val Glu Leu Leu Pro Ala Arg Glu Leu Gly Tyr
100 105 110
Asp Thr Leu Val Ile Ala Val Gly Ser Thr Thr Asn Asp Phe Gly Thr
115 120 125
Glu Gly Ala Ala Gln His Cys Leu Phe Leu Asp Thr Arg Lys Gln Ala
130 135 140
Glu Arg Phe His Gln Gln Leu Leu His His Tyr Leu Arg Ala His Ala
145 150 155 160
Gly Gln Thr Asp Ile Val Glu Arg Ile Ser Val Ala Ile Val Gly Ala
165 170 175
Gly Ala Thr Gly Val Glu Leu Ala Ala Glu Leu His Asn Ala Ala His
180 185 190
Glu Leu His Ala Tyr Gly Leu Asp Arg Ile Lys Pro Glu Asn Met His
195 200 205
Ile Thr Leu Ile Glu Ala Gly Pro Arg Val Leu Pro Ala Leu Pro Glu
210 215 220
Arg Ile Gly Gly Pro Val His Lys Thr Leu Glu Lys Leu Gly Val Asn
225 230 235 240
Val Met Thr Asn Ala Ala Val Ser Gln Val Thr Ala Asp Ser Leu Ile
245 250 255
Thr Ala Asp Gly Lys Val Ile Asp Ala Ser Leu Lys Val Trp Ala Ala
260 265 270

Gly Ile Arg Ala Pro Asp Phe Leu Lys Asp Ile Asp Gly Leu Glu Thr
275 280 285

Asn Arg Ile Asn Gln Leu His Val Leu Pro Thr Leu Gln Thr Thr Arg
290 295 300

Asp Glu Asn Ile Phe Ala Phe Gly Asp Cys Ala Ala Cys Pro Gln Pro
305 310 315 320

Gly Ser Glu Arg Asn Val Pro Pro Arg Ala Gln Ala Ala His Gln Gln
325 330 335

Ala Ser Leu Leu Ala Lys Ser Leu Lys Leu Arg Ile Glu Gly Lys Ala
340 345 350

Leu Pro Glu Tyr Lys Tyr Thr Asp Tyr Gly Ser Leu Ile Ser Leu Ser
355 360 365

Arg Phe Ser Ala Val Gly Asn Leu Met Gly Asn Leu Thr Gly Ser Val
370 375 380

Met Leu Glu Gly Trp Leu Ala Arg Met Phe Tyr Val Ser Leu Tyr Arg
385 390 395 400

Met His Gln Met Ala Leu Tyr Gly Met Phe Arg Thr Ala Met Leu Met
405 410 415

Leu Gly Ser Lys Ile Gly Arg Gly Thr Glu Pro Arg Leu Lys Leu His
420 425 430

<210> 11

<211> 1296

<212> DNA

<213> Azotobacter vinelandii

<220>

<221> CDS

<222>

<400> 11

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Met Thr His Arg Ile Val Ile Val Gly Gly Gly Ala Gly Gly Val Glu
1 5 10 15

ctc gct acc cgc ctc ggc aag acc atg ggc agg aac ttc cag gcg aag
Leu Ala Thr Arg Leu Gly Lys Thr Met Gly Arg Asn Phe Gln Ala Lys
20 25 30

atc acc ctg gtc gac gcc aac atg acc cac ctg tgg aaa ccg ctg ctg
Ile Thr Leu Val Asp Ala Asn Met Thr His Leu Trp Lys Pro Leu Leu

48

96

144

35	40	45	
cac gaa gtc gcc gcc ggc tcg ctg aac tcg acc ggc gac gaa ctg aac His Glu Val Ala Ala Gly Ser Leu Asn Ser Thr Gly Asp Glu Leu Asn 50	55	60	192
tat gtg gcc cag gcc aaa tgg aac aac ttc gag ttc cag tac ggc cgc Tyr Val Ala Gln Ala Lys Trp Asn Asn Phe Glu Phe Gln Tyr Gly Arg 65	70	75	240
atg tgc ggt ctg gac cgg gcc aac aag cgt atc cgc ctg gcg gcc cag Met Cys Gly Leu Asp Arg Ala Asn Lys Arg Ile Arg Leu Ala Ala Gln 85	90	95	288
ccg gcc cag gaa gat cgc gcg ccc ctg ccc gag cgc gaa ctg gaa tac Pro Ala Gln Glu Asp Arg Ala Pro Leu Pro Glu Arg Glu Leu Glu Tyr 100	105	110	336
gac acc ctg gtc ctt tcc gtc ggc agc acc acc aat gac ttc ggc acc Asp Thr Leu Val Leu Ser Val Gly Ser Thr Thr Asn Asp Phe Gly Thr 115	120	125	384
ccg ggc gcc gcc gag aac tgt att ttc ctg gaa ggc cgc gac cag gcc Pro Gly Ala Ala Glu Asn Cys Ile Phe Leu Glu Gly Arg Asp Gln Ala 130	135	140	432
gag cgt ttc cgc cgt ccg ctg ctc agc cac tac ttg cgt gcc cac gcc Glu Arg Phe Arg Arg Pro Leu Leu Ser His Tyr Leu Arg Ala His Ala 145	150	155	480
agc aat gac gac ggc cat cag gtc aag gtc gcc atc gtc ggc gcc ggt Ser Asn Asp Asp Gly His Gln Val Lys Val Ala Ile Val Gly Ala Gly 165	170	175	528
gcc acc ggg gtc gaa ctg gcc gca gaa ctg cgc cac gcc tcc aag gaa Ala Thr Gly Val Glu Leu Ala Ala Glu Leu Arg His Ala Ser Lys Glu 180	185	190	576
ctg gtc gcc tat ggg ctg gag cgc att ccg ccg gag aac ctc agc atc Leu Val Ala Tyr Gly Leu Glu Arg Ile Pro Pro Glu Asn Leu Ser Ile 195	200	205	624
acg ctg atc gaa tcc agc ccg cgt gta ctc gcc gcc ctg ccc gaa cgc Thr Leu Ile Glu Ser Ser Pro Arg Val Leu Ala Ala Leu Pro Glu Arg 210	215	220	672
atc agc cgc tcc gcg cac gcc acc ctg gaa agc ctg ggc gtt cgc gtg Ile Ser Arg Ser Ala His Ala Thr Leu Glu Ser Leu Gly Val Arg Val 225	230	235	720
			240

ctc	gtc	agc	acc	gcc	gtc	agc	gag	gtc	acc	gct	gaa	ggc	gtg	aag	acg	768
Leu	Val	Ser	Thr	Ala	Val	Ser	Glu	Val	Thr	Ala	Glu	Gly	Val	Lys	Thr	
245									250					255		
aag	gac	gac	cag	ttc	atc	ccc	gcc	gac	ctc	atg	gtc	tgg	gcc	gca	ggc	816
Lys	Asp	Asp	Gln	Phe	Ile	Pro	Ala	Asp	Leu	Met	Val	Trp	Ala	Ala	Gly	
260									265				270			
gtc	cgc	gct	ccc	gcc	ttc	ctc	aag	gag	ctg	gat	ggt	ctg	gaa	acc	aat	864
Val	Arg	Ala	Pro	Ala	Phe	Leu	Lys	Glu	Leu	Asp	Gly	Leu	Glu	Thr	Asn	
275							280					285				
cgc	atc	aac	cag	ttg	cag	gtc	cgc	cag	acc	ctg	cag	act	act	ctg	gac	912
Arg	Ile	Asn	Gln	Leu	Gln	Val	Arg	Gln	Thr	Leu	Gln	Thr	Thr	Leu	Asp	
290							295					300				
gac	gat	atc	ttc	gcc	ttc	ggc	gat	tgt	gcc	tcc	tgc	ccg	cag	ccg	ggt	960
Asp	Asp	Ile	Phe	Ala	Phe	Gly	Asp	Cys	Ala	Ser	Cys	Pro	Gln	Pro	Gly	
305						310				315				320		
acc	gac	cgc	ccc	gtt	ccg	ccg	cgc	gcc	cag	gcc	gct	cac	cag	cag	gcc	
1008																
Thr	Asp	Arg	Pro	Val	Pro	Pro	Arg	Ala	Gln	Ala	Ala	His	Gln	Gln	Ala	
									325		330		335			
agc	ctg	ctg	gcc	aag	tcg	ctc	cac	cgc	aag	ctg	cag	gaa	gac	agc	ctc	
1056																
Ser	Leu	Leu	Ala	Lys	Ser	Leu	His	Arg	Lys	Leu	Gln	Glu	Asp	Ser	Leu	
									340		345		350			
tgc	tgg	agt	atc	gct	aca	gct	aac	cac	ggc	tcg	ctg	atc	tcc	ctc	tcg	
1104																
Cys	Trp	Ser	Ile	Ala	Thr	Ala	Asn	His	Gly	Ser	Leu	Ile	Ser	Leu	Ser	
									355		360		365			
agc	ttc	tcg	gct	atc	ggt	aac	ctg	atg	ggc	aac	ctg	acc	ggc	aac	gtg	
1152																
Ser	Phe	Ser	Ala	Ile	Gly	Asn	Leu	Met	Gly	Asn	Leu	Thr	Gly	Asn	Val	
									370		375		380			
acc	ttg	gaa	ggc	tgg	ctg	gcc	cgc	aag	ttc	tac	att	tcc	ctg	tac	cgc	
1200																
Thr	Leu	Glu	Gly	Trp	Leu	Ala	Arg	Lys	Phe	Tyr	Ile	Ser	Leu	Tyr	Arg	
									385		390		395		400	
atg	cac	cag	atg	gct	ctc	tac	ggt	acc	ttc	cgc	acc	ctg	atg	atg	atg	
1248																
Met	His	Gln	Met	Ala	Leu	Tyr	Gly	Thr	Phe	Arg	Thr	Leu	Met	Met	Met	
									405		410		415			

ctg ggc gac cgc ttc cgc agc agc acc gaa ccc cgc ctc aag ctt cac
1296
Leu Gly Asp Arg Phe Arg Ser Ser Thr Glu Pro Arg Leu Lys Leu His
420 425 430

<210> 12
<211> 432
<212> PRT
<213> Azotobacter vinelandii

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20 25 30
Ile Thr Leu Val Asp Ala Asn Met Thr His Leu Trp Lys Pro Leu Leu
35 40 45
His Glu Val Ala Ala Gly Ser Leu Asn Ser Thr Gly Asp Glu Leu Asn
50 55 60
Tyr Val Ala Gln Ala Lys Trp Asn Asn Phe Glu Phe Gln Tyr Gly Arg
65 70 75 80
Met Cys Gly Leu Asp Arg Ala Asn Lys Arg Ile Arg Leu Ala Ala Gln
85 90 95
Pro Ala Gln Glu Asp Arg Ala Pro Leu Pro Glu Arg Glu Leu Glu Tyr
100 105 110
Asp Thr Leu Val Leu Ser Val Gly Ser Thr Thr Asn Asp Phe Gly Thr
115 120 125
Pro Gly Ala Ala Glu Asn Cys Ile Phe Leu Glu Gly Arg Asp Gln Ala
130 135 140
Glu Arg Phe Arg Arg Pro Leu Leu Ser His Tyr Leu Arg Ala His Ala
145 150 155 160
Ser Asn Asp Asp Gly His Gln Val Lys Val Ala Ile Val Gly Ala Gly
165 170 175
Ala Thr Gly Val Glu Leu Ala Ala Glu Leu Arg His Ala Ser Lys Glu
180 185 190
Leu Val Ala Tyr Gly Leu Glu Arg Ile Pro Pro Glu Asn Leu Ser Ile
195 200 205

Thr Leu Ile Glu Ser Ser Pro Arg Val Leu Ala Ala Leu Pro Glu Arg
210 215 220

Ile Ser Arg Ser Ala His Ala Thr Leu Glu Ser Leu Gly Val Arg Val
225 230 235 240

Leu Val Ser Thr Ala Val Ser Glu Val Thr Ala Glu Gly Val Lys Thr
245 250 255

Lys Asp Asp Gln Phe Ile Pro Ala Asp Leu Met Val Trp Ala Ala Gly
260 265 270

Val Arg Ala Pro Ala Phe Leu Lys Glu Leu Asp Gly Leu Glu Thr Asn
275 280 285

Arg Ile Asn Gln Leu Gln Val Arg Gln Thr Leu Gln Thr Thr Leu Asp
290 295 300

Asp Asp Ile Phe Ala Phe Gly Asp Cys Ala Ser Cys Pro Gln Pro Gly
305 310 315 320

Thr Asp Arg Pro Val Pro Pro Arg Ala Gln Ala Ala His Gln Gln Ala
325 330 335

Ser Leu Leu Ala Lys Ser Leu His Arg Lys Leu Gln Glu Asp Ser Leu
340 345 350

Cys Trp Ser Ile Ala Thr Ala Asn His Gly Ser Leu Ile Ser Leu Ser
355 360 365

Ser Phe Ser Ala Ile Gly Asn Leu Met Gly Asn Leu Thr Gly Asn Val
370 375 380

Thr Leu Glu Gly Trp Leu Ala Arg Lys Phe Tyr Ile Ser Leu Tyr Arg
385 390 395 400

Met His Gln Met Ala Leu Tyr Gly Thr Phe Arg Thr Leu Met Met Met
405 410 415

Leu Gly Asp Arg Phe Arg Ser Ser Thr Glu Pro Arg Leu Lys Leu His
420 425 430

<210> 13

<211> 1302

<212> DNA

<213> *Salmonella typhimurium* LT2

<220>

<221> CDS
<222>

<400> 13

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Met Thr Thr Pro Leu Lys Lys Ile Val Ile Val Gly Gly Gly Ala Gly
1 5 10 15

ggg ctg gaa atg gcg acg cag tta ggc cat aaa ctg ggg cgc aag aaa 96
Gly Leu Glu Met Ala Thr Gln Leu Gly His Lys Leu Gly Arg Lys Lys
20 25 30

aaa gcg aaa atc acg ctg gta gac aga aat cac agc cat ctg tgg aaa 144
Lys Ala Lys Ile Thr Leu Val Asp Arg Asn His Ser His Leu Trp Lys
35 40 45

cca ttg ctg cac gaa gtg gcg act ggc tct ctg gac gaa ggc gtg gat 192
Pro Leu Leu His Glu Val Ala Thr Gly Ser Leu Asp Glu Gly Val Asp
50 55 60

gcg ctg agc tat ctg gct cat gcg cgt aat cat ggt ttc cag ttc cag 240
Ala Leu Ser Tyr Leu Ala His Ala Arg Asn His Gly Phe Gln Phe Gln
65 70 75 80

ctg ggg tcg gtg atg gat atc gat cgc gaa gcg aaa acc atc acc att 288
Leu Gly Ser Val Met Asp Ile Asp Arg Glu Ala Lys Thr Ile Thr Ile
85 90 95

gcc gag ttg cgt gat gaa aag ggc gaa ctg ctg gtg ccg gag cgc aaa 336
Ala Glu Leu Arg Asp Glu Lys Gly Glu Leu Leu Val Pro Glu Arg Lys
100 105 110

atc gcg tat gac acg ctg gtg atg gcg ctg ggc agc acc tct aat gat 384
Ile Ala Tyr Asp Thr Leu Val Met Ala Leu Gly Ser Thr Ser Asn Asp
115 120 125

ttc aac acg ccg ggc gtg aaa gag cac tgt atc ttc ctc gat aac ccg 432
Phe Asn Thr Pro Gly Val Lys Glu His Cys Ile Phe Leu Asp Asn Pro
130 135 140

cat cag gcg cgc cgt ttt cac cag gag atg ctg aac ctg ttc ctc aag 480
His Gln Ala Arg Arg Phe His Gln Glu Met Leu Asn Leu Phe Leu Lys
145 150 155 160

tat tcg gct aat ctg ggc gcg aac ggt aag gtc aat atc gcc atc gtt 528
Tyr Ser Ala Asn Leu Gly Ala Asn Gly Lys Val Asn Ile Ala Ile Val
165 170 175

ggc ggc ggt gcg acg ggg gtt gag ctg tcg gct gaa ctg cat aat gcg	576																																																																																																
Gly Gly Gly Ala Thr Gly Val Glu Leu Ser Ala Glu Leu His Asn Ala																																																																																																	
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Val Lys Gln Leu His Ser Tyr Gly Tyr Lys Gly Leu Thr Asn Asp Ala																																																																																																	
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Pro Leu Leu His Glu Val Ala Thr Gly Ser Leu Asp Glu Gly Val Asp
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His Gln Ala Arg Arg Phe His Gln Glu Met Leu Asn Leu Phe Leu Lys
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Tyr Ser Ala Asn Leu Gly Ala Asn Gly Lys Val Asn Ile Ala Ile Val
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Gly Gly Gly Ala Thr Gly Val Glu Leu Ser Ala Glu Leu His Asn Ala
180 185 190

Val Lys Gln Leu His Ser Tyr Gly Tyr Lys Gly Leu Thr Asn Asp Ala
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Pro Leu Lys Ala Tyr Gln Tyr Lys Asp His Gly Ser Leu Val Ser Leu
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Asp Thr Val Thr Gly Ile Asp Lys Lys Ala Gln Thr Val Thr Thr Glu
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cac gga agt tat caa tat gat caa ctt tta att agt ttg ggt ggg gaa 336

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Ile	Asn	Met	Leu	Asn	Arg	Thr	Gln	Ala	Gly	Lys	Ala	Ala	Lys	Tyr	Met	
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Phe	Gly	Ile	Glu	Thr	Asn	Pro	Arg	Gly	Gly	Arg	Leu	Met	Ala	Asn	Glu	
									275					280		285
ttc	atg	caa	gct	aag	gat	tgt	aac	aat	atc	ttc	tta	gcc	ggt	gat	tca	912
Phe	Met	Gln	Ala	Lys	Asp	Cys	Asn	Asn	Ile	Phe	Leu	Ala	Gly	Asp	Ser	
									290					295		300

acc agc tac caa gaa cct gac caa cca cg_g cca gtc cca caa atc gtt 960
Thr Ser Tyr Gln Glu Pro Asp Gln Pro Arg Pro Val Pro Gln Ile Val
305 310 315 320

caa ggg gct gaa gaa acc gca gct aag gcc gtc gaa ggt att att aag 1008
Gln Gly Ala Glu Glu Thr Ala Ala Lys Ala Val Glu Gly Ile Ile Lys
325 330 335

aac gtt gac cag act gac gtt acg atc aag cca ttt aag ggc gct tat 1056
Asn Val Asp Gln Thr Asp Val Thr Ile Lys Pro Phe Lys Gly Ala Tyr
340 345 350

caa gca tcc gtc gac tca att ggt tcc aaa tat gcc gtt gca caa gtt 1104
Gln Ala Ser Val Asp Ser Ile Gly Ser Lys Tyr Ala Val Ala Gln Val
355 360 365

tta gag aag tgg aac gtc tct ggt ttt att gcc gtg ctt tta aaa cac 1152
Leu Glu Lys Trp Asn Val Ser Gly Phe Ile Ala Val Leu Leu Lys His
370 375 380

gcc atc aac tgg atg tac tac gtt cag att ttc tca ggt tac tac cta 1200
Ala Ile Asn Trp Met Tyr Tyr Val Gln Ile Phe Ser Gly Tyr Tyr Leu
385 390 395 400

ttc cag tac ttc atg cac gaa ttc ttc cgg act cgt aat aac cgt aac 1248
Phe Gln Tyr Phe Met His Glu Phe Phe Arg Thr Arg Asn Asn Arg Asn
405 410 415

gtc ttc cgc ggt tgg gtc tca cgg gct ggt aac gta ctc tgg agt gtg 1296
Val Phe Arg Gly Trp Val Ser Arg Ala Gly Asn Val Leu Trp Ser Val
420 425 430

cca ctg cgg ttc ttc tat ggt gcc atg tgg tta tgg gac tgc tgg act 1344
Pro Leu Arg Phe Phe Tyr Gly Ala Met Trp Leu Trp Asp Cys Trp Thr
435 440 445

aaa gtt cag gga tct gaa tcc tgg ttc act gac aag tta cgg tta cca 1392
Lys Val Gln Gly Ser Glu Ser Trp Phe Thr Asp Lys Leu Arg Leu Pro
450 455 460

ttc gaa tgg att acc gtg gcc gca acc agt ggt gcc tct caa gca act
1440
Phe Glu Trp Ile Thr Val Ala Ala Thr Ser Gly Ala Ser Gln Ala Thr
465 470 475 480

aaa gcc gct gca acc agt ggt gct tct gaa gct gcc acg tca acc gtt
1488
Lys Ala Ala Ala Thr Ser Gly Ala Ser Glu Ala Ala Thr Ser Thr Val
485 490 495

aaa gcc gct aag ggt gtc ttc agt ctt tca tac atg tac ggt aaa gaa
1536
Lys Ala Ala Lys Gly Val Phe Ser Leu Ser Tyr Met Tyr Gly Lys Glu
500 505 510

ccc ctg atg gtc ttt gac aaa atg cca cat tgg ttc gaa tca att acc
1584
Pro Leu Met Val Phe Asp Lys Met Pro His Trp Phe Glu Ser Ile Thr
515 520 525

aag gtc ttc att ccg aac atg caa atg gcc ctc ttc ttc cag aaa ttc
1632
Lys Val Phe Ile Pro Asn Met Gln Met Ala Leu Phe Phe Gln Lys Phe
530 535 540

atg act tgt gtt gaa atc gtc att gca tta tgt att ttc ttc gga ctc
1680
Met Thr Cys Val Glu Ile Val Ile Ala Leu Cys Ile Phe Phe Gly Leu
545 550 555 560

ttt act tgg ttt gct aac gca gtc acc att ggc tta gtt gtc gtc ttc
1728
Phe Thr Trp Phe Ala Asn Ala Val Thr Ile Gly Leu Val Val Val Phe
565 570 575

tgc tta tct ggc atg ttc tac tgg gtc aac att tgg atg atc ttt gtt
1776
Cys Leu Ser Gly Met Phe Tyr Trp Val Asn Ile Trp Met Ile Phe Val
580 585 590

gcc ctc gcc tta atg aac ggt tcc gga cgg aca ttt ggg tta gac tac
1824
Ala Leu Ala Leu Met Asn Gly Ser Gly Arg Thr Phe Gly Leu Asp Tyr
595 600 605

tgg gtc gtt ccg tgg atg caa aaa cac ctt gga cac tgg tgg tac ggc
1872
Trp Val Val Pro Trp Met Gln Lys His Leu Gly His Trp Trp Tyr Gly
610 615 620

aac gtt cgt tct cat tac gac ggt gtt aaa acc cgc
Asn Val Arg Ser His Tyr Asp Gly Val Lys Thr Arg
625 630 635

<210> 16
<211> 636
<212> PRT
<213> Lactobacillus plantarum WCFS1

<400> 16
Met Ala Lys Lys Asn Ile Val Val Val Gly Ala Gly Phe Ala Gly Val
1 5 10 15

Tyr Ala Thr Lys Lys Leu Ser Lys His Phe Lys Lys Asn Ala Asp Val
20 25 30

Glu Ile Thr Leu Ile Asp Arg His Ser Tyr Phe Thr Tyr Met Thr Glu
35 40 45

Leu His Glu Val Ala Thr Glu Arg Val Glu Pro Glu His Ile Gln Tyr
50 55 60

Asp Leu Gln Arg Leu Phe Ala Arg Arg Lys Asn Val Arg Leu Val Thr
65 70 75 80

Asp Thr Val Thr Gly Ile Asp Lys Lys Ala Gln Thr Val Thr Thr Glu
85 90 95

His Gly Ser Tyr Gln Tyr Asp Gln Leu Leu Ile Ser Leu Gly Gly Glu
100 105 110

Ser Asn Asp Phe Gly Thr Pro Gly Val Lys Glu His Gly Phe Glu Leu
115 120 125

Trp Ser Phe Glu Gln Ala Met Ala Leu Arg Ala His Leu Ser Ala Ile
130 135 140

Ile Arg Arg Gly Ala Ala Glu Leu Asp Pro Ala Lys Arg Lys Ala Met
145 150 155 160

Leu Thr Phe Thr Val Cys Gly Ser Gly Phe Thr Gly Ser Glu Leu Ile
165 170 175

Gly Glu Leu Ile Glu Tyr Arg Asp Val Leu Ala Arg Asp Asn Lys Leu
180 185 190

Asp Pro Ser Glu Ile Thr Leu Gln Leu Val Glu Ala Ala Pro Thr Ile
195 200 205

Ile Asn Met Leu Asn Arg Thr Gln Ala Gly Lys Ala Ala Lys Tyr Met

210	215	220
Glu Lys His Gly Val Lys Ile Met Thr Asn Ser Met Ile Thr Glu Val		
225	230	235
Cys Glu Asp His Val Asn Leu Lys Gly Lys Asp Pro Ile Pro Thr Tyr		
245	250	255
Thr Leu Ile Trp Thr Ala Gly Val Arg Ala Asn Ser Ile Val Lys Lys		
260	265	270
Phe Gly Ile Glu Thr Asn Pro Arg Gly Gly Arg Leu Met Ala Asn Glu		
275	280	285
Phe Met Gln Ala Lys Asp Cys Asn Asn Ile Phe Leu Ala Gly Asp Ser		
290	295	300
Thr Ser Tyr Gln Glu Pro Asp Gln Pro Arg Pro Val Pro Gln Ile Val		
305	310	315
320		
Gln Gly Ala Glu Glu Thr Ala Ala Lys Ala Val Glu Gly Ile Ile Lys		
325	330	335
Asn Val Asp Gln Thr Asp Val Thr Ile Lys Pro Phe Lys Gly Ala Tyr		
340	345	350
Gln Ala Ser Val Asp Ser Ile Gly Ser Lys Tyr Ala Val Ala Gln Val		
355	360	365
Leu Glu Lys Trp Asn Val Ser Gly Phe Ile Ala Val Leu Leu Lys His		
370	375	380
Ala Ile Asn Trp Met Tyr Tyr Val Gln Ile Phe Ser Gly Tyr Tyr Leu		
385	390	395
400		
Phe Gln Tyr Phe Met His Glu Phe Phe Arg Thr Arg Asn Asn Arg Asn		
405	410	415
Val Phe Arg Gly Trp Val Ser Arg Ala Gly Asn Val Leu Trp Ser Val		
420	425	430
Pro Leu Arg Phe Phe Tyr Gly Ala Met Trp Leu Trp Asp Cys Trp Thr		
435	440	445
Lys Val Gln Gly Ser Glu Ser Trp Phe Thr Asp Lys Leu Arg Leu Pro		
450	455	460
Phe Glu Trp Ile Thr Val Ala Ala Thr Ser Gly Ala Ser Gln Ala Thr		
465	470	475
480		

Lys Ala Ala Ala Thr Ser Gly Ala Ser Glu Ala Ala Thr Ser Thr Val
485 490 495

Lys Ala Ala Lys Gly Val Phe Ser Leu Ser Tyr Met Tyr Gly Lys Glu
500 505 510

Pro Leu Met Val Phe Asp Lys Met Pro His Trp Phe Glu Ser Ile Thr
515 520 525

Lys Val Phe Ile Pro Asn Met Gln Met Ala Leu Phe Phe Gln Lys Phe
530 535 540

Met Thr Cys Val Glu Ile Val Ile Ala Leu Cys Ile Phe Phe Gly Leu
545 550 555 560

Phe Thr Trp Phe Ala Asn Ala Val Thr Ile Gly Leu Val Val Val Phe
565 570 575

Cys Leu Ser Gly Met Phe Tyr Trp Val Asn Ile Trp Met Ile Phe Val
580 585 590

Ala Leu Ala Leu Met Asn Gly Ser Gly Arg Thr Phe Gly Leu Asp Tyr
595 600 605

Trp Val Val Pro Trp Met Gln Lys His Leu Gly His Trp Trp Tyr Gly
610 615 620

Asn Val Arg Ser His Tyr Asp Gly Val Lys Thr Arg
625 630 635